SEQUENCE LISTING

<110> Basi, Guriq
Saldanha, Jose
Yednock, Ted

<120> Humanized Antibodies that Recognize
Beta-Amyloid Peptide

<130> ELN-002

<150> 60/251,892
<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 396
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(396)

<221> sig_peptide
<222> (1)...(60)

<400> 1

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atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg   48
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20                 -15                 -10                  -5

gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg   96
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
                1               5                   10

gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc   144
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15                  20                  25

ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg   192
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
    30                  35                  40

cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac   240
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45                  50                  55                  60

tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt   288
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
```

```
aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat   336
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
             80                  85                  90

tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag   384
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
         95                  100                 105

ctg gaa atc aaa                                                   396
Leu Glu Ile Lys
    110
```

<210> 2
<211> 132
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(20)

<400> 2

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Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20                 -15                 -10                 -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
                 1                   5                  10
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15                  20                  25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
    30                  35                  40
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45                  50                  55                  60
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
            80                  85                  90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
        95                  100                 105
Leu Glu Ile Lys
    110
```

<210> 3
<211> 414
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(414)

<221> sig_peptide
<222> (1)...(57)

<400> 3

atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt 48
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
-15 -10 -5

gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag 96
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
1 5 10

cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc 144
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25

agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg 192
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
30 35 40 45

gag tgg gtt gca tcc att agg agt ggt ggt ggt aga acc tac tat tca 240
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
50 55 60

gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac 288
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
65 70 75

acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg 336
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
80 85 90

tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg 384
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
95 100 105

ggc cag ggc acc act gtc aca gtc tcc tca 414
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115

<210> 4
<211> 138
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 4
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
-15 -10 -5
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
1 5 10
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
30 35 40 45

```
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
            65                  70                  75
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
        80                  85                  90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                  100                 105
Gly Gln Gly Thr Thr Ile Thr Val Ser Ser
110                 115
```

<210> 5
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 5

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Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20                 -15                 -10                 -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
                 1                   5                  10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15                  20                  25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
    30                  35                  40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45                  50                  55                  60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105
Val Glu Ile Lys
    110
```

<210> 6
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 6

```
Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
                -15                 -10                 -5
Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
             1                   5                  10
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
    15                  20                  25
Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
30                  35                  40                  45
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
                50                  55                  60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
            65                  70                  75
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
        80                  85                  90
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
    95                  100                 105
```



```
<210> 7
<211> 100
<212> PRT
<213> Homo sapiens

<400> 7
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1               5                  10                  15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20                  25                  30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95
Leu Gln Thr Pro
            100


<210> 8
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 3D6 heavy chain variable region

<221> SIGNAL
<222> (1)...(19)

<400> 8
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
                -15                 -10                 -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
             1                   5                  10
```

```
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                  20                  25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
            65                  70                  75
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
        80                  85                  90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                  100                 105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110                 115
```

<210> 9
<211> 121
<212> PRT
<213> Homo sapiens

<400> 9

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95
Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 10
<211> 98
<212> PRT
<213> Homo sapiens

<400> 10

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys

<210> 11
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20 -15 -10 -5
Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
1 5 10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
15 20 25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
30 35 40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45 50 55 60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
65 70 75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105
Val Glu Ile Lys
110

<210> 12
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 3D6 light chain variable region

<221> SIGNAL
<222> (1)...(19)

<400> 12
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
-15 -10 -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25

```
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
            65                  70                  75
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
        80                  85                  90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                  100                 105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110                 115
```

<210> 13
<211> 393
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(393)

<221> sig_peptide
<222> (1)...(57)

<400> 13

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atg aag ttg cct gtt agg ctg ttg gta ctg atg ttc tgg att cct gct   48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
                -15                 -10                 -5

tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc   96
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            1               5                   10

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag aac att   144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
     15                  20                  25

ata cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca   192
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
 30                  35                  40                  45

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct   240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
                50                  55                  60

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca   288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            65                  70                  75

ctc aag atc aag aaa gtg gag gct gag gat ctg gga att tat tac tgc   336
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
        80                  85                  90
```

```
ttt caa ggt tca cat gtt ccg ctc acg ttc ggt gct ggg acc aag ctg   384
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
     95                  100                 105

gag ctg gaa                                                      393
Glu Leu Glu
110
```

<210> 14
<211> 131
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 14

```
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
                -15                 -10                 -5
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
             1                   5                  10
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
    15                  20                  25
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
30                  35                  40                  45
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
                50                  55                  60
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            65                  70                  75
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
        80                  85                  90
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
    95                  100                 105
Glu Leu Glu
110
```

<210> 15
<211> 426
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(426)

<221> sig_peptide
<222> (1)...(57)

<400> 15

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atg gac agg ctt act tcc tca ttc ctg ctg ctg att gtc cct gca tat   48
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
               -15                 -10                 -5
```

```
gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag   96
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
            1               5                  10

tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg   144
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
     15                  20                  25

agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag   192
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 30                  35                  40                  45

ggt ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat   240
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
                50                  55                  60

aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga   288
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
            65                  70                  75

aag cag gta ttc ctc aag atc acc agt gtg gac cct gca gat act gcc   336
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
         80                  85                  90

aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct   384
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
     95                  100                 105

atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca           426
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110                 115                 120
```

<210> 16
<211> 142
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 16

```
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
                -15                 -10                 -5
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
            1               5                  10
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
    15                  20                  25
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
30                  35                  40                  45
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
                50                  55                  60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
            65                  70                  75
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
```

```
        80                  85                  90
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
    95                  100                 105
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110                 115                 120
```

<210> 17
<211> 136
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
tccgcaagct tgccgccacc atggacatgc gcgtgcccgc ccagctgctg ggcctgctga 60
tgctgtgggt gtccggctcc tccggctacg tggtgatgac ccagtccccc ctgtccctgc 120
ccgtgacccc cggcga 136

<210> 18
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
ctggggggac tggccgggct tctgcagcag ccagttcagg taggtcttgc cgtcggagtc 60
cagcagggac tgggaggact tgcaggagat ggaggcgggc tcgccggggg tcacgggcag 120
ggacaggggg g 131

<210> 19
<211> 146
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
acctgaactg gctgctgcag aagcccggcc agtcccccca gcgcctgatc tacctggtgt 60
ccaagctgga ctccggcgtg cccgaccgct tctccggctc cggctccggc accgacttca 120
ccctgaagat ctcccgcgtg gaggcc 146

<210> 20
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
aattctagga tccactcacg cttgatctcc accttggtgc cctggccgaa ggtgcggggg 60
aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120
ttcagggtga agtcggtgcc gg 142

<210> 21
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ctgggggggac tggccg 16

<210> 22
<211> 22
<212> DNA
<<213> Artificial Sequence

<220>
<223> Primer

<400> 22
acctgaactg gctgctgcag aa 22

<210> 23
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
acagaaagct tgccgccacc atggagtttg ggctgagctg gctttttctt gtggctattt 60
taaaaggtgt ccagtgtgag gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg 120
gcggctccct gcgcctgt 138

<210> 24
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gccgccggag cggatggagg ccacccactc caggcccttg ccgggggcct ggcgcaccca 60
ggacatgccg tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcagggagcc 120
gccgggctgc accag 135

<210> 25
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
ctggagtggg tggcctccat ccgctccggc ggcggccgca cctactactc cgacaacgtg 60
aagggccgct tcaccatctc ccgcgacaac gccaagaact ccctgtacct gcagatgaac 120
tccctgcgcg ccgaggacac cg 142

<210> 26
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
ctgcaaggat ccactcaccg gaggacacgg tcaccagggt gccctggccc cagtagtcgg 60
aggagccgga gtagtggtcg tagcgcacgc agtagtacag ggcggtgtcc tcggcgcgca 120
gggagttcat ctgcaggtac aggg 144

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 27
gccgccggag cggatg 16

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 28
ctggagtggg tggcctccat 20

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 29
tccgcaagct tgccgccac 19

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 30
aattctagga tccactcacg cttgatctc 29

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 31
acagaaagct tgccgccacc atg 23

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32
ctgcaaggat ccactcaccg ga 22

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> internal peptide

<400> 33
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
1 5 10

<210> 34
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VL

<400> 34
atggacatgc gcgtgcccgc ccagctgctg ggcctgctga tgctgtgggt gtccggctcc 60
tccggctacg tggtgatgac ccagtccccc ctgtccctgc ccgtgacccc cggcgagccc 120
gcctccatct cctgcaagtc ctcccagtcc ctgctggact ccgacggcaa gacctacctg 180
aactggctgc tgcagaagcc cggccagtcc ccccagcgcc tgatctacct ggtgtccaag 240
ctggactccg gcgtgcccga ccgcttctcc ggctccggct ccggcaccga cttcaccctg 300
aagatctccc gcgtggaggc cgaggacgtg ggcgtgtact actgctggca gggcacccac 360
ttcccccgca ccttcggcca gggcaccaag gtggagatca ag 402

<210> 35
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 2 VL

<400> 35
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aactggctgc tgcagaagcc cggccagtcc ccccagcgcc tgatctacct ggtgtccaag 240
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ggcaagggcc tggagtgggt ggcctccatc cgctccggcg gcggccgcac ctactactcc 240
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cagatgaact ccctgcgcgc cgaggacacc gccctgtact actgcgtgcg ctacgaccac 360
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			20					25					30		
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
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65					70					75					80
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
				85					90					95	
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val
			100					105					110		
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
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Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
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Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
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Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
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Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
			180					185					190		
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
		195					200					205			
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
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Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
225					230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
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Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
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Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
		275					280					285			
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
	290					295					300				
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
305					310					315					320
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
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Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr
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Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala
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Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460
Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495
Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560
Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575
Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590
Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605
Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620
Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640
Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670
Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720
Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
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